



QY 424 VDRNRNQVIAAGCGGGUGLMLGFLILTVKLHQPLKATVFNNSSLGMVKLEMUVEQPEFGT 483

Db 425 TDRRQVQVMSMGDFMLMGDFLWHDLPVKTFLVNNSLGMVELEMVAGLPSHG 484

QY 484 DHEEVNFAEIAAAGIKSVRTPDKVREQLAELAAYPGVLDIVTPNALSITPTW 543

Db 485 ANKNPDPFAAVAEAGAFAFGVRYEKKPLKOLAGAKAFAFRHKGALVDPNALSITPTW 543

QY 544 EQWMGISAATRTVFGGVGAMIDLARSNTNTP 579

Db 545 DMVGFPLASKVILDGGVGVMLQMASRNLNRP 580

QY 60 SLITGELAVQAAASCOPGNPHLIGQYDSRNGAKWIAKSAQISSTFEEAHPIL 119

Db 61 AQLSGELAVQAGSCPGNPHLIGQYDSRNGAKWIAKSAQISSTFEEAHPIL 120

DEE CPC

Pyruvate dehydrogenase (cytochrome) (EC 1.2.2.2) - Escherichia coli

N; Alternate names: pyruvate oxidase

C; Species: Escherichia coli

C; Accession: A23641; G6425; I55291; I57856

R; Grabau, C.; Cronan, Jr., J.E.

Nucleic Acids Res. 14, 5449-5460, 1986

A; Title: Nucleotide sequence and deduced amino acid sequence of Escherichia coli pyruvate

A; Reference number: A23648; MUID: 80286555

A; Accession: A23648

A; Molecule type: DNA

A; Residues: 1-572 <GRA>

A; Cross-references: GB:x04105; GB:MT13947; GB:MT13948; NID:942472; PIDN:CAA27725.1; PID:942472

A; Experimental source: strain K-12

R; Lattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A; Title: The complete genome sequence of Escherichia coli K-12.

A; Reference number: A64720; MUID:97426617

A; Status: nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA

A; Residues: 1-572 <BLAT>

A; Cross-references: GB:AE000188; GB:U00096; NID:91787084; PIDN:ACT73958.1; PID:91787096;

A; Experimental source: strain K-12, substrain MG1655

R; Grabau, C.; Chang, Y.Y.; Cronan, J.E.

J. Biol. Chem. 264, 12510-12519, 1989

A; Title: Lipid binding by Escherichia coli pyruvate oxidase is disrupted by small altera

A; Reference number: 155291; MUID:89308683

A; Address: 155291

A; Status: translated from GB/EMBL/DDJB

A; Residues: 1-363, 'HE', 366-413, 'HCV', 417-572 <RES>

A; Experimental source: strain K-12

R; Chang, Y.Y.; Wang, A.Y.; Cronan, J.E.

Mol. Microbiol. 11, 1019-1028, 1994

A; Title: Expression of Escherichia coli pyruvate oxidase (PoxB) depends on the sigma fac

A; Reference number: 157856; MUID:94239372

A; Molecule type: DNA

A; Status: translated from GB/EMBL/DDJB

A; Residues: 1-22 <RES>

A; Cross-references: GB:573268; NID:9685127; PIDN:AAB31180.1; PID:9685128

C; Comment: The sequence of this protein was shown to be homologous with those of the lar

C; Comment: Pyruvate is the end product.

C; Comment: This protein is not to be confused with a similar enzyme, pyruvate (or pyruvi

C; Comment: ion) of pyruvate to acetyl phosphate, carbon dioxide, and hydrogen peroxide.

C; Comment: C-glycans.

A; Gene: poxB

A; Map position: 19 min

C; Complex: homotetramer

C; Function:

A; Description: catalyzes the conversion of pyruvate to acetate and carbon dioxide in the

A; Note: in the presence of pyruvate and cofactor thiamine pyrophosphate, the addition of

C; Superfamily: acetylactate syntase large chain; thiamin pyrophosphate-binding domain

C; Keywords: FAD; flavoprotein; homotetramer; lipid binding; magnesium; membrane protein; F432-470/Domain: thiamin pyrophosphate-binding domain homology <TPB>

F;50/Active site: Glu #status predicted

Query Match 44.1%; Score 1317.5; DB 1; Length 572;

Best Local Similarity 46.3%; Pred. No. 1.3e-78; Mismatches 195; Indels 7; Gaps 6;

Matches 266; Conservative 106; Mismatches 195; Indels 7; Gaps 6;

Db 1 MAHSYAEQLDITLQEQVKLYLGVGSNLPITVAV-RQSDIEWVHVNREAAFAAGAE 59

Db 1 MKQTWAVIYKILLESAGVKRWVGDLSLNSRNGTIEWMSTRHEEVAFAGAE 60

QY 60 SLITGELAVQAAASCOPGNPHLIGQYDSRNGAKWIAKSAQISSTFEEAHPIL 119

Db 61 AQLSGELAVQAGSCPGNPHLIGQYDSRNGAKWIAKSAQISSTFEEAHPIL 120

DEE CPC

Pyruvate dehydrogenase (cytochrome) (EC 1.2.2.2) - Escherichia coli

N; Alternate names: pyruvate oxidase

C; Species: Escherichia coli

C; Accession: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 05-Nov-1999

R; Grabau, C.; Cronan, Jr., J.E.

Nucleic Acids Res. 14, 5449-5460, 1986

A; Title: Nucleotide sequence and deduced amino acid sequence of Escherichia coli pyruvate

A; Reference number: A23648; MUID: 80286555

A; Accession: A23648

A; Molecule type: DNA

A; Residues: 1-572 <GRA>

A; Cross-references: GB:x04105; GB:MT13947; GB:MT13948; NID:942472; PIDN:CAA27725.1; PID:942472

A; Experimental source: strain K-12

R; Lattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A; Title: The complete genome sequence of Escherichia coli K-12.

A; Reference number: A64720; MUID:97426617

A; Status: nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA

A; Residues: 1-572 <BLAT>

A; Cross-references: GB:AE000188; GB:U00096; NID:91787084; PIDN:ACT73958.1; PID:91787096;

A; Experimental source: strain K-12, substrain MG1655

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J. Biol. Chem. 264, 12510-12519, 1989

A; Title: Lipid binding by Escherichia coli pyruvate oxidase is disrupted by small altera

A; Reference number: 155291; MUID:89308683

A; Address: 155291

A; Status: translated from GB/EMBL/DDJB

A; Residues: 1-363, 'HE', 366-413, 'HCV', 417-572 <RES>

A; Experimental source: strain K-12

R; Chang, Y.Y.; Wang, A.Y.; Cronan, J.E.

Mol. Microbiol. 11, 1019-1028, 1994

A; Title: Expression of Escherichia coli pyruvate oxidase (PoxB) depends on the sigma fac

A; Reference number: 157856; MUID:94239372

A; Molecule type: DNA

A; Status: translated from GB/EMBL/DDJB

A; Residues: 1-22 <RES>

A; Cross-references: GB:573268; NID:9685127; PIDN:AAB31180.1; PID:9685128

C; Comment: The sequence of this protein was shown to be homologous with those of the lar

C; Comment: C-glycans.

A; Gene: poxB

A; Map position: 19 min

C; Complex: homotetramer

C; Function:

A; Description: catalyzes the conversion of pyruvate to acetate and carbon dioxide in the

A; Note: in the presence of pyruvate and cofactor thiamine pyrophosphate, the addition of

C; Superfamily: acetylactate syntase large chain; thiamin pyrophosphate-binding domain

C; Keywords: FAD; flavoprotein; homotetramer; lipid binding; magnesium; membrane protein; F432-470/Domain: thiamin pyrophosphate-binding domain homology <TPB>

QY 424 VDRNRNQVIAAGCGGGUGLMLGFLILTVKLHQPLKATVFNNSSLGMVKLEMUVEQPEFGT 483

Db 425 TDRRQVQVMSMGDFMLMGDFLWHDLPVKTFLVNNSLGMVELEMVAGLPSHG 484

QY 484 DHEEVNFAEIAAAGIKSVRTPDKVREQLAELAAYPGVLDIVTPNALSITPTW 543

Db 485 ANKNPDPFAAVAEAGAFAFGVRYEKKPLKOLAGAKAFAFRHKGALVDPNALSITPTW 543

QY 544 EQWMGISAATRTVFGGVGAMIDLARSNTNTP 579

Db 545 DMVGFPLASKVILDGGVGVMLQMASRNLNRP 580

QY 60 SLITGELAVQAAASCOPGNPHLIGQYDSRNGAKWIAKSAQISSTFEEAHPIL 119

Db 61 AQLSGELAVQAGSCPGNPHLIGQYDSRNGAKWIAKSAQISSTFEEAHPIL 120

DEE CPC

Pyruvate dehydrogenase (cytochrome) (EC 1.2.2.2) - Escherichia coli

N; Alternate names: pyruvate oxidase

C; Species: Escherichia coli

C; Accession: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 05-Nov-1999

R; Grabau, C.; Cronan, Jr., J.E.

Nucleic Acids Res. 14, 5449-5460, 1986

A; Title: Nucleotide sequence and deduced amino acid sequence of Escherichia coli pyruvate

A; Reference number: A23648; MUID: 80286555

A; Accession: A23648

A; Molecule type: DNA

A; Residues: 1-572 <GRA>

A; Cross-references: GB:x04105; GB:MT13947; GB:MT13948; NID:942472; PIDN:CAA27725.1; PID:942472

A; Experimental source: strain K-12

R; Lattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A; Title: The complete genome sequence of Escherichia coli K-12.

A; Reference number: A64720; MUID:97426617

A; Status: nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA

A; Residues: 1-572 <BLAT>

A; Cross-references: GB:AE000188; GB:U00096; NID:91787084; PIDN:ACT73958.1; PID:91787096;

A; Experimental source: strain K-12, substrain MG1655

R; Grabau, C.; Chang, Y.Y.; Cronan, J.E.

J. Biol. Chem. 264, 12510-12519, 1989

A; Title: Lipid binding by Escherichia coli pyruvate oxidase is disrupted by small altera

A; Reference number: 155291; MUID:89308683

A; Address: 155291

A; Status: translated from GB/EMBL/DDJB

A; Residues: 1-22 <RES>

A; Cross-references: GB:573268; NID:9685127; PIDN:AAB31180.1; PID:9685128

C; Comment: The sequence of this protein was shown to be homologous with those of the lar

C; Comment: C-glycans.

A; Gene: poxB

A; Map position: 19 min

C; Complex: homotetramer

C; Function:

A; Description: catalyzes the conversion of pyruvate to acetate and carbon dioxide in the

A; Note: in the presence of pyruvate and cofactor thiamine pyrophosphate, the addition of

C; Superfamily: acetylactate syntase large chain; thiamin pyrophosphate-binding domain

C; Keywords: FAD; flavoprotein; homotetramer; lipid binding; magnesium; membrane protein; F432-470/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Qy 6 AEQOLIDLEAQWKWKRIVGLGVGDSLNP1YDAVRSIDIEWHRNEAAFAAGAESLITGE 65  
 ||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:  
 Db 7 AEIVVETELLEAVGRHICGIVGDTLNUVTDIHSQTSOWHVRHEAAFAAGAESLITGR 66

Qy 66 LAVCAASCGPGNHLIQLGQYDLSHNRGAKVLTATSHPSAQISTFFOETPHELFKECS 125  
 ||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:  
 Db 67 LTACAGSCGPGLSLHFINGVYEAQRNRPWLIJASQITPQLGMEFPOEVDFKAVYASCSV 126

Qy 126 YCEMVNGEGERILHIAOSTMAGKVSVWIPGDIAKEDADGDTYSNSTISGGTV 185  
 ||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:  
 Db 127 FCEQVHREPEQARRVVALACQAAINRRGAVVWILPADIQSATVKKDLD--PFSTHPQDVLR 184

Qy 186 PDPTEAALVAEINNAKSVTLECCAGVKNARAQVLEAKIKSPIGHALGGQYQIHENP 245  
 ||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:  
 Db 185 PSDNLDVQDVARLAHKGKIGIAAGSCGQAHLLVADRLKAPANTSRAKDFEVYDNP 244

Qy 246 FEQMSGLLGYGACVADASNEADLLILGLDFPVSDFLP-KDNVAQDINGAHIGRTTV 304  
 ||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:  
 Db 245 FNGMGTGMLGIESGFHMTECDTLLLGADFAWAQFPOKATLIVQDRGSHLRRHPID 304

Qy 305 KPYVTGDVATIENILPVAKEKTDRLMLKAHERK-----LSSVVEYTIN 352  
 ||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:  
 Db 305 LGVVGVDVATIGALLPKLKARTDRAYIDACL-AHYRKAREGDELPPASRDASPFTN 364

RESULT 5

G69769

pyruvate oxidase homolog ydap - *Bacillus subtilis*

C;Species: *Bacillus subtilis*

C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Jun-2000

C;Accession: G69769

R;Kunst, P.; Ogasawa, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; C.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabre, C.; Ferrari, A.; Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hisano, S.; Hullo, M.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, M.; Levine, R.; Liu, H.; Masuda, S.; Mau Y.; Ogawa, K.; Ogiwara, K.; Oudega, B.; Park, V.; Pohl, T.M.; Porte Rieger, M.; Rivalta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scani A.; Authors: Schleifer, S.; Schneiter, R.; Scipione, F.; Sekiguchi, J.; Sekowska, A.; Seakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Tepstra, P.; Toonon, A.; Tosato, V.; Uchiy T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*

A;Reference number: A69580; MUID:98044033

A;Accession: G69769

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-574 <KUN>

C;Accession: S01682

C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 15-Oct-1999

R;Ammura, A.; Fujita, M.; Futa, M.

R;Submitted to the EMBL Database, November 1988

A;Description: Amino acid sequence of a protein by a region downstream of the isoamylase Escherichia coli.

A;Reference number: S01681.

A;Accession: S01682

A;Molecule type: DNA

A;Residues: 1-396 <AM2>

A;Cross-references: EMBL:X13378; NID:945380; PIDN:CAA31755.1; PID:945382

A;Experimental source: strain SB-15

A;Note: the source is designated as *Pseudomonas amylocladomosa*

C;Keywords: FAD; flavoprotein; lipid binding; magnesium; membrane protein; oxidoreductase

F;51/active site: Glu #status predicted

Query Match 30.2%; Score 902.5; DB 2; Length 396; Best Local Similarity 49.0%; PRED. NO. 1.1e-51; Matches 176; Conservative 72; Mismatches 98; Indels 13; Gaps 4; Matches 198; Conservative 120; Mismatches 242; Indels 20; Gaps 10;

Qy 1 MAHYSYAEQ-LIDITTLEAQWKWKRIVGLGVGDSLNP1YDAVRSIDIEWHRNEAAFAAG 57  
 ||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:  
 Db 1 MAHKTAGQAMTELLEQWVQDHVVGIPGQSSINETEELRHERNQKFIOTRHEEVAA 60

Qy 58 AESLUTGEMDVAASCSPGNTLHQGLDSHNRGAKVLAISHPAQSAGSTFOETIPE 117  
 ||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:  
 Db 61 AERKLIGKIVCLSIAGPAVHLGLYDADGAPVLAQVAGQSSGEVGRDFQEIKE 120

Qy 118 LIRKECSYCEMVNGEGERILHIAOSTMAGKVSVWIPD -AKEDADGDTYSNT 176  
 ||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:  
 Db 121 QMFEDVAVFVNREVHSAESLDPDNLQATRTAYSKRGVAVLSVSDLFKEKIKRPVYTSV 180

Qy 177 ISSTGPVVFDPTEAALVAEINNAKSVTLECCAGVKNARAQVLEAKIKSPIGHALGG 236  
 ||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:  
 Db 181 YIEGN - -LEPKKEQOLVTCAQYINNAKKPITIAGQGMKKAKRELEFADKAAPIVWTLPA 238



RESULT	9
C69059	
acetolactate synthase (EC 4.1.3.18) large chain - <i>Methanobacterium thermoautotrophicum</i>	
C:Species: <i>Methanobacterium thermoautotrophicum</i>	
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999	
C:Accession: C69059	
R:Smith, D.R.; Boucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafina, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Javan, I.; Kl, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.	
J: Bacteriol. 179, 7135-7155, 1997	
A:Title: Complete genome sequence of <i>Methanobacterium thermoautotrophicum</i> Delta	
A:Reference number: A69000; MUID:98037514	
A:Accession: C69059	
A:Status: Preliminary; nucleic acid sequence not shown; translation not shown	
A: Molecule type: DNA	
A: Residues: 1-577 <MTH>	
A: Cross-references: GI: AE000666; NID:92622541; PIDN:AABB8591.1; PID:92622556	
A: Experimental source: strain Delta H	
C:Genetics:	
A:Gene: MTH444	
A:Start codon: GCG	
C:Superfamily: acetolactate synthase large chain; thiamin pyrophosphate-binding domain	
C:Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase; flavoprotein	
F:428-476/Domain: thiamin pyrophosphate-binding domain homology <TPB>	

Db	482	YDQVKTITLNGWGMVRQWQFYERYASNSMSQMP-----DINL--LCEAYGI	533
Qy	500	KSVRITDPKVREQDLEALAYPGVPLIDWT--DPNAL-SIPTITWQVGMGSKAATR	555
Db	533	KGITVKKREDLAPAIEMLAHNGPVMDVWVKKDENCYPMIAPGMSNAQMLGLPVEPV	591
Db	539	EILPMVPPGCLTEIVG	555
RESULT	10		
S75115			
acetoxy acid synthase - Synechocystis sp. (strain PCC 6803)			
N; Alternate names: protein slr2088			
C; Species: Synechocystis sp.			
A; Variety: PCC 6803			
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000			
C; Accession: S75115			
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O.; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA; 3, 109-136, 1995			
A; Title: Sequencing analysis of the genome of the unicellular cyanobacterium Synechocystis			
A; Reference number: S74332; MUID:97061201			
A; Accession: S75115			
A; Status: nucleic acid sequence not shown; translation not shown			
A; Molecule type: DNA			
A; Residues: 1-621 <KAN>			
A; Cross-references: EMBL:D90910; GB:AB001339; NID:9162956; PIDN:BA017977.1; PID:9165306			
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996			
C; Genetics:			
A; Gene: ilvG			
A; Start codon: GTG			
C; Superfamily: acetoacetate synthase large chain: thiamin pyrophosphate-binding domain			
Query Match	19.0%	Score 567; DB 2; Length 621;	
Best Local Similarity	27.4%	Pred. No. 1.8e-29; Mismatches 113; Indels 236; Gaps 18;	
Matches	164;	Conservative 113; Mismatches 236; Indels 86; Gaps 18;	
Qy	9	LIDTLEAQVKRIGVINGVLSNLPVDAVRO---SDIIEWHVRNEAAFAAGAESLTG	64
Db	27	LMDLSLRKRGVHKHCGPGPAGLPLPYDELRFEAEGEIELHVRMFGQASHADQYARATG	86
Qy	65	ELAVCAASCAGPGNTHIQLQGDYDSDHRSRNGAKVLAISHPSAQIGSTFFOE-----THPEI	118
Db	87	KVGWCFGTSGFGATNLVGTGIANAHLDHSVPMVWVQVGRAMIGSDAQDFOIDIFGTLPIV	146
Qy	119	LFKECSGYCMVNGEQQGEILHHAQSTMAGK-GVSVVWPGDIAKE-----DAGD	170
Db	147	-----KHSVVRSAADMARIVTSAFHLASTGRPGVPLIDPKVGLVSECEYIFLPDGD	199
Qy	171	TYSNISTISSTPVPVFPDPPEAAVLYEAVINNAKSTLFCGAG- VKNARAQVLEAKTKS	228
Db	200	-----VNLPGYRPTVKGPNRQINAALQLEQARNLQYLPGVNLQYGGAAIANAHQAQVQEAEQL	255
Qy	229	PIGHALGGKROYIQHENPFENGMSCLIGYACVDSNEADLILIGTDF-----PYSDFL	282
Db	256	PVTTILMIGGAFDENHPLPSVGMGLMHGHTAYANFAVSECIDLAVGARFDDRVTKRLDEFA	315
Qy	283	PKDQWVQAQDINGAIGRRTVKGPTVGDVAATENILPHVKE-----KTDSEFLDRM	335
Db	316	SAKVIHIDPDAVGVKNRAPDVPIVGDVRLFQQLRARELYDPTPHPTQAWLNR	373
Qy	4	SVAQDILDTLEAQVKRIGVLDGDSLNPIVDAVRQSDIIEWHVRNEAAATAAGAESLT	63
Db	19	SGALMLIESLKKVEMIFGVGGAVAPIKYKLNSGLVHLPRHQGAIHAEYGARVS	78
Qy	64	GELAVCAASCAGPGNTHIQLQGDYDSDHRSRNGAKVLAISHPSAQIGSTFFOEIHPETL	123
Db	79	GKPGWVIASTGPGATNLVGTGADAMIDSPLVWVFTGQVATSVIGSDAQEIDLGLITMPV	138
Qy	124	SGCENMNGGEGERILHHAQSTMAGK-GVSVVWPGDIAKEDAGDTYSNSTISSG-T	181
Db	139	TKSYQVQRPEDLPRIKAFHJATTGPGVPLIDIPKDVAIE-GEFSYDHMNLPGY	197
Qy	392	YIENPEGTRDFVGSSFRHGMANALPHA1GAQSVDRNROVIAMCGGGLGMLGELFLVVL	451
Db	424	FLNN-GPWRWISSAGLGLTMGFLPAMGAKVGVGDCAVICISGDAFQMLQELGLTQA	481
Qy	452	HQPLKAVVNNNSLGMVK-----LEMLVQCPETDHEVNFALAAAGI	499
Qy	240	TOHENPFEVGMMSGILGSGYACVVDASNEADLILLGTDPP-----YSDFLPDPDNQAVDIN	293

RESULT 12

T1197 acetohydroxyacid synthase large subunit - red alga (Cyanidium caldarium) chloroplast  
 C;Species: chloroplast; Cyanidium caldarium  
 C;Accession: T1197  
 R;Gloeckner, G.; Rosenthal, A.; Valentin, K.  
 submitted to the EMBL Data Library, September 1997  
 A;Description: Organisation of 46 kb of the Cyanidium caldarium RKL plastid genome.  
 A;Reference number: 217374  
 A;Accession: T1197  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-585 <GLO>  
 A;Cross-references: EMBL:AF022186; NID:92465730; PIDN:AAB82660.1; PID:92465731  
 A;Experimental source: strain RKL  
 C;Genetics:  
 A;Genome: chloroplast  
 A;Note: 11VB  
 C;Superfamily: acetolactate synthase large chain; thiamin pyrophosphate-binding domain  
 F;446-494/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 18.4% Score 549; DB 2; Length 585;  
 Best Local Similarity 27.3%; Pred. No. 2. 5e-28; Matches 160; Conservative 112; Mismatches 247; Indels 68; Gaps 15;

Query 9 LIDLTLEAQVGRVYGLVGSDSLNPPIAVW---RQSDIEWVHVRNEAAFAAGAESLITG 64  
 Db 16 LIDMLVYKVKVKNIFGPGGATLPIPYDELHYWEKKLKLHYLVRHEGSAAHANDAYARAT 75

Qy 65 ELAVCAASCGGCGTNTLIGLYDHSRNGAKVLAISHPAQSIGSTFFQETIPELKECS 124  
 Db 76 EVGVLCLATSGPGATNLVYGLTQAMDSVPIIAITGOSRAFIGTDAFOQEVQIFGIRLPIV 135

Qy 125 GYCEMNGGEOCERILHQAOSTMACK-GVSVVWPGDIAKEDAG---DGTYNSNTISS 179  
 Db 136 KHSFVVRDPRETIIVSEAFVSKHGRPGAVLIDVKGLEEFNHYDYSIRDHKPITK 195

Qy 180 GPPVVFDPTEAALVAEINNAKSVTLFCAGVKNRAQ--VLELAEKIKSPIGHALGGK 237  
 Db 196 YRPVYGPSIROIEKFRMLLESKQPIVYGGGAVMSRAQHEIEELASFPIKIPVTTLMGK 255

Qy 238 QYIQUHENPFEVGMGSLGLGYGACVADASNEADLLILGTD----PYSDELPKDNQAQVD 291

Db 256 GSPNEYNPPLYLGMLGHHGKTYAANFAVSECDDLLIAALGAREFDDRTGKLEDEFACNAQYTHD 315

Qy 292 INGAMIGRRTVVKYPVTDGVAVATIENILPHVKEKTDORSFLDRMLKAHERKLSSVWETYTH 351  
 Db 316 IDPAAEIGKNRIPQALATISDIKIVKLSSMKETNN--MDK-----NQPAWLH 363

Qy 352 NVEK-----HV-----IHPYVYVASYILNEELADKDAVFTVDTGMCNVHARYIENPEGT 399

RESULT 13

A44857 acetolactate synthase (EC 4.1.3.18) - *Spirulina platensis*  
 C;Species: *Spirulina platensis*  
 C;Accession: A44857  
 R;Milano, A.; De Rossi, E.; Zanaria, E.; Barblerato, L.; Ciferri, O.; Riccardi, J. Gen. Microbiol. 138, 139-148, 1992  
 A;Title: Molecular characterization of the genes encoding acetohydroxy acid synthase  
 A;Reference number: A44857; MUID:92381487  
 A;Accession: A44857  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-612 <ML>  
 A;Note: sequence extracted from NCBI backbone (NCBN:112275, NCBI:112276)  
 C;Superfamily: acetolactate synthase large chain; thiamin pyrophosphate-binding domain  
 C;Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase; oxo-acid-lyase  
 F;446-494/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 18.3% Score 546; DB 2; Length 612;  
 Best Local Similarity 26.6%; Pred. No. 4. 2e-28; Matches 164; Conservative 123; Mismatches 253; Indels 76; Gaps 19;

Query 6 AEQOLIDTLEAQVGRVYGLVGSDSLNPPIAVW---AVROSDIEWVHVRNEAAFAAGAESL 61  
 Db 15 AFLRIDSURKHQHQVHIFGPGGAILPYDELHYRAEAGDIQHILVRHQASHADGYR 74

Qy 62 ITGELAVCAASCGGCGTNTLIGLYDHSRNGAKVLAISHPAQSIGSTFFQETIPELKECS 134

Db 75 ATGRGVGCFGTSGPGATNLVYGLTQAMDSVPIIAITGOSRAFIGTDAFOQEVQIFGIRLPIV 135

Qy 115 ---HPEITLKFCKSGVCEMWNGEQE---RILHHAOSTMACK-GVSVVWPGDIAKED- 166  
 Db 135 PIVKHSVWV-----REPGDMARVIAEFAHISASGRGPGVPLDVPKDVGLEEF 181

Qy 167 ---AGBDYTSNISTISGGTPVFPDTEAALVAEINNAKSVTLFCAGV--KNRAQVL 220  
 Db 182 DYIPVNNGEVS--LGYRPTVKGNYRQINQIKLIEEARPLMYVGGASATANERIA 238

Qy 221 ELAEKIKSPIGHALGGKQYIOTHENPFEVGMGSLLGYGACVADASNEADLLILGTD---- 276  
 Db 239 ELAEFLQIPTVTTLMGKSFDEKPLSVMGLGMHGTYAYANFVASECDDFLAVGAREFDDV 298

Qy 277 --PYSDELPKDNQAQVDINGAHIGRRTVVKYPVTDGVAVATIENILPHVKEKTD---- 327  
 Db 299 TCKLDRFGSKRVIHIDPAEVGKNTPEVPIVGDVQVOLIHLRRCRIGDGVNDNT 358

Qy 328 RSFLDRMLKAHERKLSSVWETYTHVNEKHPYVYVASYILNEELADKDAVFTVDTGMCNV 387

Db 359 QSWLERINRNPW-DYPLWPSDS---LSPQEVIAELGKMA-PDGYYTIDVQHOM 410

Db 299 TCKLDRFGSKRVIHIDPAEVGKNTPEVPIVGDVQVOLIHLRRCRIGDGVNDNT 358

Qy 388 WHARYIENPEGTDRFVGSFRHGTMANALPHVAGQSVDNRQVIAVCGGGGMLGMLGELL 447  
 Db 411 WAOFLKN--GPRQWISSAGLGMGIPGAMGKVALERSQVICINGDASVQMNQIOLG 468

Qy 448 TVKLHQLPLKAVVFNNSLGMVKEMLVEGQPEFGTDHEEV--NFAEIAAGIKSVI 504

RESULT 14

Db 469 TIAQGINVKIVIINNGWQAVRQWQAFQYERYSASNMEIGMPDFEMLARSYGVKGMV 528

Qy 505 TDPKKYREQLAEALAYPGPVILD---IVTDNNA---SIPPTTWEQMGFS---KAATR 555

Db 529 KSRDEHQAELAEMLADGPVIMDVHPTKDENCPYPMWAPGRSNQAMIGLPPERQLEKAVEL 588

Qy 557 VFGGGVGAMIDLARS 572

Db 589 IYCSNGGAK-NVASNN 603

RESULT 15

Db 475 INNAYLGMQRQWELFYDQRYSEVDLSVQPD-----FVKLAEAMGAVGMRRAKKP 525

Qy 509 KREQLAEALAYPG-PVLDIVTD---PNALIIP 539

Db 526 EVREYEEAKRIDERPVVIFDWWREENYLPMVP 559

Query Match 17.9%; Score 533.5; DB 2; Length 585;

Best Local Similarity 27.4%; Pred. No. 2.6e-27;

Matches 157; Conservative 111; Mismatches 245; Indels 61; Gaps 13;

Qy 6 AEQLIDTLEAQGVKRVIGLVGDSLNPVIDAV-RQSDIENWHRNEEAFAAGAESLITG 64

Db 7 ADIVIETLKAEGVETVFLGPAGAIMEVYDALYRIGGIKHILARHOGAGHMAEYKANG 66

Qy 65 BLAVCAASCAGPNTHLIOQYDISHRNGAKVLAISHPSAQIGSTFFQETHEPLFKECS 124

Db 67 KVGVWVNTSPPGATNLUVTPIDAVMDSVPLVATGQVPHLIGDAQFQEVDIRGIRTP 126

Qy 125 GYCEMWNGGQGERILHHAQSTIMAGK-GSVVWVPGDIAKEDAGDGTYNSNLISSG 64

Db 127 KHNFLVKSIEELPLILIREAFYIARTGRGPVFLVLPDKYDQIAVLFPSDEEVKAALPG 186

Qy 184 VFP---DPPEAAALVEATNNAKSVTLFGAGVWNRAQ---VLELAEKIKSPIGHALGK 237

Db 187 YKPHVEGNPQOKIKAELMSAKRVLVYGGAVNSEAOELIELAELMQLQIVPVT 246

Qy 238 QYIHOHENPFEVGMGSLIGLIGACVDAASNEADLILGTD-----PYSDFLPKDNV 291

Db 247 GAFTPETHPLSLRMGMHGTVYANHVNDSLIAVARGDPRVKGIDFAPGAKIHD 306

Qy 292 INGAHAGRRTTVKPVVTGDAATENILPHKEKUDRSFLDRMKAHERKLSSVET 351

Db 307 IDPASISKNTIVDPPIVGDKVIRVLRKLINEIKKG---AKTILYPEER----KMLE 355

Qy 352 NVERKWPVH-----PEVASTINELAKDQAVFTVDPGMCNTWHRVYENPEGRDFVOSFR 399

Db 356 QIEKWKKLHPLTYRNDSKVTKPOVIEQWLWEATNGEALIVPGVQOHOMAAMFYK-KYP 414

Qy 400 RDFGFSFRGTMALPHAGAQSYDRNQVIAAMGDDGLGMLGELLTIVKLHQPLKAVVFNNSLG 459

Db 415 ROFTNSGGLGMGTLPGAGIKRGPDRVEWVWDGSEFVMMQEVITAVQVKPVKVA 474

Qy 460 VENNSSLGAVK-----LMLVEGQPERFTDHEEVNFAAIAAAGIKSVRITDPK 508

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Job time: 2596 sec

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